Patent Claims

1. Method for the multidimensional analysis of a proteome in which the biological material with the proteome to be analyzed is solubilized and the proteins belonging to the proteome are separated, quantitatively determined and identified, characterized in that the proteins of the proteome are subjected to a number n of different separating processes for n>2 under standardized conditions in such a way that each of the liquid fractions m_1 obtained in a separating step supplies m_2 liquid fractions in a subsequent separating step, wherein, after n separating steps, there are $m_1 * m_2 * \ldots m_n = M$ liquid fractions which are identified by τ different analysis processes qualitatively and/or quantitatively by identification processes, known per se, and determined quantitatively by quantification processes which are likewise known per se, so that after combining the analysis data an n-dimensional image of the proteome is obtained which is characterized by identifiers and quantifiers and by the position in the n-dimensional data space.

2. Method according to claim 1, characterized in that methods which separate according to the size of the protein and/or methods which separate according to the mass of the protein and/or methods which separate according to the charge of the protein and/or methods which separate according to the hydrophobicity of the protein and/or methods which separate according to the shape of the protein and/or methods which separate according to the affinity of the protein, with respect to specific ligands, also to antibodies are selected as separating methods.

3. Method according to claim 1, characterized in that methods for determining specific immunological characteristics and/or methods for determining specific catalytic activity and/or methods for determining chemical modification of the proteins of the proteome are used as identification methods.

4. Method according to claim 1, characterized in that methods for nonspecific determination of protein concentration with different sensitivities

and/or quantitative determination methods for determining specific catalytic activities and/or quantitative immunological methods and/or quantitative binding assays are selected as quantification methods.

5. Method according to claim 1, characterized in that the identification of individual proteins of the proteome is carried out directly by mass determination of the proteins.

6. Method according to claim 1, characterized in that the identification of individual proteins is carried out according to protease digestion and mass identification of fragments.

7. Method according to claim 1, characterized in that after the separation step the fractions are assembled in a two-dimensional multiple vessel system, preferably in the manner of and with the layout of microtitration plates.

8. Method according to claim 1, characterized in that in the first separating step the fractions are assembled in a defined grid, preferably in the n * 96 grid of microtitration technology.

9. Method according to claim 1, characterized in that all identification and quantification steps are carried out in a defined grid, preferably in the n * 96 grid, with adaptable liquid handling technique.

10. Method according to claim 9, characterized in that all identification steps and quantification steps are carried out with at least four two-dimensionally arranged, simultaneously working pipettor channels.

11. Method according to claim 1, characterized in that the first dimension for separation is high-resolution size exclusion, ion exchange or hydrophobicity chromatography, which are known per se, in that the second dimension is carried out by parallel separation and fractionation of the fractions of

the first dimension by means of a principle of separation other than that used for the first dimension, and in that each further separation and fractionation is carried out by parallel separating and fractionating methods with the fractions obtained from the preceding separating and fractionating steps.

12. Method according to claim 1, characterized in that the analysis data for the n-dimensional image of the protein are assembled in a database.